

PEPTIDES PRODUCED BY *IN VITRO* DIGESTION OF CAPRINE WHEY PROTEINS: IDENTIFICATION BY NANO-LC Q-TOF

Ellen K. Eriksen¹, Einar Jensen², Halvor Holm³, Morten Jacobsen⁴, Tove G. Devold¹ and Gerd E. Vegarud¹.

¹Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, PO Box 5003, 1432 Ås, Norway

² Department of Pharmacy, University of Tromsø, 9037-Tromsø, Norway

³Institute of Nutrition, University of Oslo, Rikshospitalet and Radiumhospitalet University Hospital, 0027 Oslo, Norway

⁴Oestfold Hospital Trust and University of Oslo, Norway

Goat whey proteins were digested in two steps to simulate gastric and duodenal digestion. Gastric digestion was simulated using either human gastric juice (HGJ) or porcine pepsin A at three different pH values. During simulated duodenal digestion either human duodenal juice (HDJ) or corolase PP (porcine pancreatic enzymes) was used at pH 8. The degradation profiles of the whey proteins were compared by SDS PAGE and the peptides produced were identified by nano-LC Q-TOF.

The higher the pH in the first step of the hydrolysis (simulated gastric digestion), the less degraded were the final hydrolysates. The porcine enzymes seemed to be more efficient at degrading the proteins especially at pH 2 in the first step, even though the enzyme activities were kept constant. pH 6 during the simulated gastric digestion resulted in poor protein degradation.

Different peptides seem to be produced depending on whether human or porcine enzymes were used as found by LC-MS/MS identification.